



SEQUENCE LISTING

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<120> IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
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<170> PatentIn Ver. 2.1

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Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys Asp
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aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc tgt 144
Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
35 40 45

aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt tat 192
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50 55 60

ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta aag 240
Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
65 70 75 80

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aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288
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35 40 45

Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe Tyr
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Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
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 65 70 75 80

 aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288
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 Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
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 Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe Tyr
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 Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
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 35 40 45

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 65 70 75 80

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 35 40 45

 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
 50 55 60

 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
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 35 40 45
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 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe
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 Tyr Leu Ser Asp Cys Asn Ala Thr Ser Arg Pro Cys Lys Tyr Lys Leu
 65 70 75 80
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 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
 35 40 45
 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Phe Glu Phe
 50 55 60

B1
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Tyr Leu Ser Asp Cys Asn Ala Thr Ser Arg Pro Cys Lys Tyr Lys Leu
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 35 40 45
 Glu Pro Val Lys Ala Ile Cys Lys Gly Ile Ile Ala Ser Lys Asn Val
 50 55 60
 Leu Thr Thr Ser Glu Phe Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg
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 20 25 30

B!
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Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
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aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt tat 192
Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe Tyr
      50              55              60

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Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
      65              70              75

aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca gta 288
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Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile Cys
      35              40              45

Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe Tyr
      50              55              60

Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu Lys
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 Asp Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys
 20 25 30

 gac aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc 144
 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
 35 40 45

 tgt aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt 192
 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
 50 55 60

 tat ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta 240
 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
 65 70 75 80

 aag aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca 288
 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
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 35 40 45

 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
 50 55 60

 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
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 atc tgc aac act atc atg gac aac aac atc tac atc gtt ggt ggt cag 96
 Ile Cys Asn Thr Ile Met Asp Asn Asn Ile Tyr Ile Val Gly Gly Gln
 20 25 30
 tgc aaa cgt gtt aac act ttc atc atc tct tct gct act act gtt aaa 144
 Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val Lys
 35 40 45
 gct atc tgc act ggt gtt atc aac atg aac gtt ctg tct act act cgt 192
 Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr Arg
 50 55 60
 ttc cag ctg aac act tgc act cgt act tct atc act ccg cgt ccg tgc 240
 Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro Cys
 65 70 75 80
 ccg tac tct tct cgt act gaa act aac tac atc tgc gtt aaa tgc gaa 288
 Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys Glu
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 Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val Lys
 35 40 45
 Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr Arg
 50 55 60

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atc atc tgc aac act atc atg gac aac aac atc tac atc gtt ggt ggt 96
Ile Ile Cys Asn Thr Ile Met Asp Asn Asn Ile Tyr Ile Val Gly Gly
20 25 30

cag tgc aaa cgt gtt aac act ttc atc atc tct tct gct act act gtt 144
Gln Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val
35 40 45

aaa gct atc tgc act ggt gtt atc aac atg aac gtt ctg tct act act 192
Lys Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr
50 55 60

cgt ttc cag ctg aac act tgc act cgt act tct atc act ccg cgt ccg 240
Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro
65 70 75 80

tgc ccg tac tct tct cgt act gaa act aac tac atc tgc gtt aaa tgc 288
Cys Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys
85 90 95

gaa aac cag tac ccg gtt cat ttc gct ggt atc ggt cgt tgc ccg 333
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 35 40 45
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 Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro
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 Ile Cys Asn Thr Ile Leu Asp Asn Asn Ile Tyr Ile Val Gly Gly Gln
 20 25 30
 tgc aaa cgt gtt aac act ttc atc atc tct tct gct act act gtt aaa 144
 Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val Lys
 35 40 45
 gct atc tgc act ggt gtt atc aac ctg aac gtt ctg tct act act cgt 192
 Ala Ile Cys Thr Gly Val Ile Asn Leu Asn Val Leu Ser Thr Thr Arg
 50 55 60
 ttc cag ctg aac act tgc act cgt act tct atc act ccg cgt ccg tgc 240
 Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro Cys
 65 70 75 80
 ccg tac tct tct cgt act gaa act aac tac atc tgc gtt aaa tgc gaa 288
 Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys Glu
 85 90 95

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 Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val Lys
 35 40 45
 Ala Ile Cys Thr Gly Val Ile Asn Leu Asn Val Leu Ser Thr Thr Arg
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 Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro Cys
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 Ile Ile Cys Asn Thr Ile Leu Asp Asn Asn Ile Tyr Ile Val Gly Gly
 20 25 30
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 Gln Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val
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cgt ttc cag ctg aac act tgc act cgt act tct atc act ccg cgt ccg 240
 Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro
 65 70 75 80

tgc ccg tac tct tct cgt act gaa act aac tac atc tgc gtt aaa tgc 288
 Cys Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys
 85 90 95

gaa aac cag tac ccg gtt cat ttc gct ggt atc ggt cgt tgc ccg 333
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 20 25 30

Gln Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val
 35 40 45

Lys Ala Ile Cys Thr Gly Val Ile Asn Leu Asn Val Leu Ser Thr Thr
 50 55 60

Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro
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Ile Tyr Ile Val Gly Gly Gln Cys Lys Arg Val Asn Thr Phe Ile Ile
 35 40 45
 Ser Ser Ala Thr Thr Val Lys Ala Ile Cys Thr Gly Val Ile Asn Leu
 50 55 60
 Asn Val Leu Ser Thr Thr Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr
 65 70 75 80
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 atc tgc aac act atc atg gac aac aac atc tac atc gtt ggt ggt cag 96
 Ile Cys Asn Thr Ile Met Asp Asn Asn Ile Tyr Ile Val Gly Gly Gln
 20 25 30
 tgc aaa cgt gtt aac act ttc atc atc tct tct gct act act gtt aaa 144
 Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val Lys
 35 40 45
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 Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr Arg
 50 55 60
 ttc cag ctg aac act tgc act cgt act tct atc act ccg cgt ccg tgc 240
 Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro Cys
 65 70 75 80
 ccg tac tct tct cgt act gaa act aac tac atc tgc gtt aaa tgc gaa 288
 Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys Glu
 85 90 95
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 <213> Rana catesbeiana

<400> 24
 Ser Asn Trp Ala Thr Phe Gln Gln Lys His Ile Ile Asn Thr Pro Ile
 1 5 10 15
 Ile Cys Asn Thr Ile Met Asp Asn Asn Ile Tyr Ile Val Gly Gly Gln
 20 25 30
 Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val Lys
 35 40 45
 Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr Arg
 50 55 60
 Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro Cys
 65 70 75 80
 Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys Glu
 85 90 95
 Asn Gln Tyr Pro Val His Phe Ala Gly Ile Gly Arg Cys Pro
 100 105 110

B
 <210> 25
 <211> 333
 <212> DNA
 <213> Rana catesbeiana

<220>
 <221> CDS
 <222> (1)..(333)

<400> 25
 atg tca aac tgg gct act ttc cag cag aaa cat atc atc aac act ccg 48
 Met Ser Asn Trp Ala Thr Phe Gln Gln Lys His Ile Ile Asn Thr Pro
 1 5 10 15
 atc atc tgc aac act atc atg gac aac aac atc tac atc gtt ggt ggt 96
 Ile Ile Cys Asn Thr Ile Met Asp Asn Asn Ile Tyr Ile Val Gly Gly
 20 25 30
 cag tgc aaa cgt gtt aac act ttc atc atc tct tct gct act act gtt 144
 Gln Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val
 35 40 45
 aaa gct atc tgc act ggt gtt atc aac atg aac gtt ctg tct act act 192
 Lys Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr
 50 55 60
 cgt ttc cag ctg aac act tgc act cgt act tct atc act ccg cgt ccg 240
 Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro
 65 70 75 80

gaa aac cag tac ccg gtt cat ttc gct ggt atc ggt cgt tgc ccg 333
Glu Asn Gln Tyr Pro Val His Phe Ala Gly Ile Gly Arg Cys Pro
100 105 110

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<210> 26
<211> 111
<212> PRT
<213> Rana catesbeiana
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<400> 26
Met Ser Asn Trp Ala Thr Phe Gln Gln Lys His Ile Ile Asn Thr Pro
1 5 10 15

Ile Ile Cys Asn Thr Ile Met Asp Asn Asn Ile Tyr Ile Val Gly Gly
20 25 30

Gln Cys Lys Arg Val Asn Thr Phe Ile Ile Ser Ser Ala Thr Thr Val
35 40 45

Lys Ala Ile Cys Thr Gly Val Ile Asn Met Asn Val Leu Ser Thr Thr
50 55 60

Arg Phe Gln Leu Asn Thr Cys Thr Arg Thr Ser Ile Thr Pro Arg Pro
65 70 75 80

Cys Pro Tyr Ser Ser Arg Thr Glu Thr Asn Tyr Ile Cys Val Lys Cys
85 90 95

Glu Asn Gln Tyr Pro Val His Phe Ala Gly Ile Gly Arg Cys Pro
100 105 110

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<210> 27
<211> 2855
<212> DNA
<213> Rana pipiens
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<220>
<221> CDS
<222> (97) .. (477)
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<400> 27
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tctcttatat ataaaggcct gatcacgact tccaga atg ttt cca aaa ttc tca 114
Met Phe Pro Lys Phe Ser
1 5

t t t c t c c t g a t a t t t g c a g t t g t t t t g a g t c t c a c t c a t a a g t c c t t a 162
Phe Leu Leu Ile Phe Ala Val Val Leu Ser Leu Thr His Lys Ser Leu
10 15 20

tgt caa gac tgg ctt acg ttt cag aag aag cac ctg aca aac acc cgg 210
 Cys Gln Asp Trp Leu Thr Phe Gln Lys Lys His Leu Thr Asn Thr Arg
 25 30 35

gat gtt gac tgt aat aat atc atg tca aca aac ttg ttc cac tgc aag 258
 Asp Val Asp Cys Asn Asn Ile Met Ser Thr Asn Leu Phe His Cys Lys
 40 45 50

gac aag aac act ttt atc tat tca cgt cct gag cca gtg aag gcc atc 306
 Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro Glu Pro Val Lys Ala Ile
 55 60 65 70

tgt aaa gga att ata gcc tcc aaa aat gtg tta act acc tct gag ttt 354
 Cys Lys Gly Ile Ile Ala Ser Lys Asn Val Leu Thr Thr Ser Glu Phe
 75 80 85

tat ctc tct gat tgc aat gta aca agc agg cct tgc aag tat aaa tta 402
 Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg Pro Cys Lys Tyr Lys Leu
 90 95 100

aag aaa tca act aat aca ttt tgt gta act tgt gag aat caa gct cca 450
 Lys Lys Ser Thr Asn Thr Phe Cys Val Thr Cys Glu Asn Gln Ala Pro
 105 110 115

gta cat ttc gtg ggt gtc gga cat tgc tagaaatg tttgacaaca 497
 Val His Phe Val Gly Val Gly His Cys
 120 125

gggatgtgat aagcagctgc aagaaattat tttgaagtga atttactaaa gacactaatt 557
 ttgcataaat tttccccaga gcttaccggt agtaagaaaa ttccaacagg gagccaagca 617
 cagaaagtaa actaaggagc caaagtaatt ataaaagtca cactggaccg ctgctactgc 677
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 aggtggcggg gagtcaattg gggatggagt ccatgtgaga tttggaaccg tttgttgctg 797
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B1

gttggttcct tgccacctcc tggatctgtg ctttccaatt ctgttttttc cccagcgctt 1457
 agtggatgca gtgaaactct ggtgattacc atcatccaat catgtgcaag aaaaaatatt 1517
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<210> 28
 <211> 127
 <212> PRT
 <213> Rana pipiens

<400> 28

Met Phe Pro Lys Phe Ser Phe Leu Leu Ile Phe Ala Val Val Leu Ser
 1 5 10 15

Leu Thr His Lys Ser Leu Cys Gln Asp Trp Leu Thr Phe Gln Lys Lys
 20 25 30

His Leu Thr Asn Thr Arg Asp Val Asp Cys Asn Asn Ile Met Ser Thr
 35 40 45

Asn Leu Phe His Cys Lys Asp Lys Asn Thr Phe Ile Tyr Ser Arg Pro
 50 55 60

Glu Pro Val Lys Ala Ile Cys Lys Gly Ile Ile Ala Ser Lys Asn Val
 65 70 75 80

Leu Thr Thr Ser Glu Phe Tyr Leu Ser Asp Cys Asn Val Thr Ser Arg
 85 90 95

Pro Cys Lys Tyr Lys Leu Lys Lys Ser Thr Asn Thr Phe Cys Val Thr
 100 105 110

Cys Glu Asn Gln Ala Pro Val His Phe Val Gly Val Gly His Cys
 115 120 125

<210> 29

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 CAAX motif

<400> 29

Cys Val Ile Met
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<210> 30

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

agrgatgatk attgygataa yatcatg

27

<210> 31

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

aaartgmacw ggkgcctgrt tytcaca

27

<210> 32

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 32

cagaactggg ctactttcca gcagaaacat atcatcaaca ctccgatcat ctgcaacact 60
atcatggaca acaacatcta catcgttggt ggtcag 96

<210> 33

<211> 86

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 33

tacatcggtg gtggtcagtg caaacgtgtt aacactttca tcactctctt gctactactg 60
ttaaactgat ctgcactggt gttatc 86

<210> 34

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 34

atctgcactg gtgttactaa catgaacgtt ctgtctacta ctcgtttcca gctgaacact 60
tgcaactgta cttctatcac tccgcgtccg tgcccg 96

<210> 35

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotideB1
ck

<400> 35
gttgataaca ccagtgacaga t 21

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 36
atctgcactg gtgttatcaa c 21

<210> 37
<211> 95
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 37
actccgcgtc cgtgcccgta ctcttctcgt actgaaacta actacatctg cgtaaatagc 60
gaaaaccagt acccggttca ttctgctggt atcgg 95

<210> 38
<211> 71
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 38
atatatctag aaataatttt atttaacttt aagaaggaga tatacatatg cagaactggg 60
ctactttcca g 71

<210> 39
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 39
cgcgccggat ccctactacg ggcaacgacc gataccagcg aaatgaac 48

B1
if

<210> 40
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 40
 cagaactggg ctactttcca gcagaaacat atcatcaaca ctccgatcat ctgcaacact 60
 atcctgcaga acaacatcta catcggtggt ggtcag 96

<210> 41
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 41
 atctgcactg gtgttatcaa cctgaacggt ctgtctacta ctcgtttcca gctgaacact 60
 tgcactcgta cttctatcac tccgcgtccg tgcccg 96

<210> 42
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 42
 ggattccata tgcagaactg ggctattttc cag 33

<210> 43
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 6X His tag

<400> 43
 His His His His His
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